



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/913631

Source: PCT

Date Processed by STIC: 08/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/913631

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

may
The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

BEST AVAILABLE COPY

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,631

DATE: 08/30/2001

TIME: 07:45:04

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Output Set: N:\CRF3\08302001\I913631.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Theragene Biomedical Laboratories GmbH

5 <120> TITLE OF INVENTION: Hormone-Hormone Receptor Complexes and Nucleic Acid

6 Constructs and Their Use in Gene Therapy

8 <130> FILE REFERENCE: 000065wo/JH/ml

C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/913,631

C--> 11 <141> CURRENT FILING DATE: 2001-08-16

See page 1 of 7 and
page 5 of 7

13 <160> NUMBER OF SEQ ID NOS: 10

15 <170> SOFTWARE: PatentIn Ver. 2.1

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 5753

19 <212> TYPE: DNA

20 <213> ORGANISM: Artificial Sequence

W--> 22 <220> FEATURE:

W--> 22 <223> OTHER INFORMATION:

A 213 response of "Artificial Sequence"
requires explanation or description in
field 223.The type of errors shown ^{may} exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

22 <400> SEQUENCE: 1

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PATENT APPLICATION: US/09/913,631

DATE: 08/30/2001

TIME: 07:45:04

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191 acctacagcg tgagctatga gaaagcgcca cgcttccga agggagaaa ggcgacaggt 3720
192 atccggtaag cggcaggggtc ggaacaggag agcgacagag ggagcttcca ggggaaacg 3780
193 cctggtatct ttatagtcct gtcgggtttc gccacctctg acttgagcgt cgatttttgt 3840
194 gatgctcgtc agggggggcg agcctatgga aaaacgccag caacgcggcc tttttacggt 3900
195 tcttggcctt ttgctggcct tttgtctaca tgttctttcc tgcgttatcc cctgattctg 3960
196 tggataaccg tattaccgcc tttgagtgag ctgataccgc tcgccgcagc cgaacgaccg 4020
197 agcgcagcga gtcagtgage gaggaagcgg aagagcgccc aatacgaaa ccgcctctcc 4080
198 ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac tggaaagcgg 4140
199 gcagtgagec caacgcaatt aatgtgagtt agctcactca ttaggcaccc caggctttac 4200
200 actttatgct tccggtcgt atgttgtgtg gaattgtgag cggataacaa tttcacacag 4260
201 gaaacagcta tgaccatgat tacgccaagc tctctagagc tctagagctc tagagctcta 4320
202 gagagcttgc atgcctgcag gtcg
4344
205 <210> SEQ ID NO: 3
206 <211> LENGTH: 78
207 <212> TYPE: DNA

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/913,631

DATE: 08/30/2001
 TIME: 07:45:04

Input Set : A:\000065wo.app
 Output Set: N:\CRF3\08302001\I913631.raw

208 <213> ORGANISM: Artificial Sequence
 210 <220> FEATURE:
 211 <223> OTHER INFORMATION: Description of Artificial Sequence: vector pTGFG36 *OK*
 213 <400> SEQUENCE: 3
 214 ggggtaccag cttcgtagct agaacatcat gttctgggat atcagcttcg tagctagaac 60
 215 atcatgttct ggtacccc 78
 218 <210> SEQ ID NO: 4
 219 <211> LENGTH: 78
 220 <212> TYPE: DNA
 221 <213> ORGANISM: Artificial Sequence
 223 <220> FEATURE:
 224 <223> OTHER INFORMATION: Description of Artificial Sequence: vector pTGFG36 *good*
 226 <400> SEQUENCE: 4
 227 ggggtaccag aacatgatgt tctagctacg aagctgatat ccagaacat gatgttctag 60
 228 ctacgaagct ggtacccc 78
 231 <210> SEQ ID NO: 5
 232 <211> LENGTH: 19
 233 <212> TYPE: DNA
 234 <213> ORGANISM: Artificial Sequence
 W--> 236 <220> FEATURE:
 W--> 236 <223> OTHER INFORMATION: *Errored*
 236 <400> SEQUENCE: 5
 237 agcttgacct cgagcaagc 19
 240 <210> SEQ ID NO: 6
 241 <211> LENGTH: 19
 242 <212> TYPE: DNA
 243 <213> ORGANISM: Artificial Sequence
 245 <220> FEATURE:
 246 <223> OTHER INFORMATION: Description of Artificial Sequence: vector pTGFG36
 248 <400> SEQUENCE: 6
 249 ggccgcttgc tcgaggtca 19
 252 <210> SEQ ID NO: 7
 253 <211> LENGTH: 43
 254 <212> TYPE: DNA
 255 <213> ORGANISM: Artificial Sequence
 257 <220> FEATURE:
 258 <223> OTHER INFORMATION: Description of Artificial Sequence: vector pTGFG36
 260 <400> SEQUENCE: 7
 261 ggaattccgc aaaggttatg cagcgcgtga acatgatcat ggc 43
 264 <210> SEQ ID NO: 8
 265 <211> LENGTH: 39
 266 <212> TYPE: DNA
 267 <213> ORGANISM: Artificial Sequence
 269 <220> FEATURE:
 270 <223> OTHER INFORMATION: Description of Artificial Sequence: vector pTGFG36
 272 <400> SEQUENCE: 8
 273 cgcggatcca ttaagtgagc tttgtttttt ccttaatcc 39
 276 <210> SEQ ID NO: 9
 277 <211> LENGTH: 933

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/913,631

DATE: 08/30/2001

TIME: 07:45:05

Input Set : A:\000065wo.app

Output Set: N:\CRF3\08302001\I913631.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:22 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:236 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:236 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: